	A- Analysis of ANIm and TETRA among the strains sharing specific name and for which a type strain is present (T)	TETRA	ANIm	TETRA	ANIm	TETRA	ANIm
T	Acidithiobacillus ferrooxidans ATCC 23270	/	/				
	Acidithiobacillus ferrooxidans ATCC 53993	0.99876	99.62				
T	Anaeromyxobacter dehalogenans 2CP-1	/	/				
	Anaeromyxobacter dehalogenans 2CP-C	**0.99945**	**93.49**				
	Bacillus cereus 03BB102	**0.99903**	**91.98**				
	Bacillus cereus AH187	**0.99884**	**92.15**				
	Bacillus cereus AH820	**0.99891**	**92.03**				
	Bacillus cereus ATCC 10987	**0.99902**	**91.96**				
T	Bacillus cereus ATCC 14579	/	/				
	Bacillus cereus B4264	0.99968	98.16				
	Bacillus cereus E33L	**0.99899**	**91.97**				
	Bacillus cereus G9842	0.99932	95.98				
	Bacillus cereus Q1	**0.99889**	**92.12**				
	Bacillus cereus subsp. cytotoxis NVH 391-98	**0.97949**	**85.33**				
	Note: only strains B424 and G9842 belong to the same genospecies as the type strain						
T	Bacteroides fragilis NCTC 9343	/	/				
	Bacteroides fragilis YCH46	0.99947	99.17				
T	Bifidobacterium animalis subsp. lactis Bl-04	/	/				
	Bifidobacterium animalis subsp. lactis DSM 10140	1	99.97				
	Bifidobacterium_animalis_lactis_AD011	0.99993	99.95				
T	Borrelia burgdorferi B31	/	/				
	Borrelia burgdorferi ZS7	0.99198	97.59				
T	Burkholderia cenocepacia J2315	/	/	0.99948	95.08		
	Burkholderia cenocepacia AU 1054	0.99948	95.09	/	/		
	Burkholderia cenocepacia HI2424	0.99951	95.1	0.99992	99.82		
	Burkholderia cenocepacia MC0-3	0.99923	95.06	0.99962	97.92		
T	Burkholderia mallei ATCC 23344	/	/				
	Burkholderia mallei NCTC 10229	0.99997	99.8				
	Burkholderia mallei NCTC 10247	0.99997	99.79				
	Burkholderia mallei SAVP1	0.9999	99.82				
T	Caulobacter crescentus CB15	/	/				
	Caulobacter crescentus NA1000	0.99999	99.95				
	Chlamydophila pneumoniae AR39	/	/				
	Chlamydophila pneumoniae CWL029	0.99988	99.95				
	Chlamydophila pneumoniae J138	0.99986	99.95				
T	Chlamydophila pneumoniae TW-183	0.99984	99.95				
	Chlamydia trachomatis 434/Bu	/	/				
T	Chlamydia trachomatis A/HAR-13	0.99936	99.08				
	Chlamydia trachomatis D/UW-3/CX	0.99931	99.14				
	Chlamydia trachomatis L2b/UCH-1/proctitis	0.99996	99.94				
T	Chlorobium phaeobacteroides DSM 266	/	/				
	Chlorobium phaeobacteroides BS1	**0.94269**	**87.72**				
T	Clostridium kluyveri DSM 555	/	/				
	Clostridium kluyveri NBRC 12016	0.99995	99.88				
T	Clostridium perfringens ATCC 13124	/	/				
	Clostridium perfringens SM101	0.99649	97.15				
	Clostridium perfringens str. 13	0.99917	98.47				
T	Corynebacterium glutamicum ATCC 13032 (bielefeld)	/	/				
	Corynebacterium glutamicum ATCC 13032 (kitasato)	0.99997	99.92				
	Corynebacterium glutamicum R	0.99827	97.67				
T	Desulfitobacterium hafniense DCB-2	/	/				

	Desulfitobacterium hafniense Y51	0.9989	98.3
T	Desulfovibrio vulgaris str. Hildenborough	/	/
	Desulfovibrio vulgaris str. 'Miyazaki F'	**0.78034**	**83.73**
	Desulfovibrio vulgaris DP4	0.99972	98.77
	Ehrlichia ruminantium str. Gardel	0.99908	97.58
T	Ehrlichia ruminantium str. Welgevonden (UPSA)	/	/
	Ehrlichia ruminantium str. Welgevonden (CIRAD)	0.99989	99.9
	Legionella pneumophila str. Corby	0.99877	96.75
	Legionella pneumophila str. Lens	0.99884	96.83
	Legionella pneumophila str. Paris	0.99866	96.95
T	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	/	/
T	Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'	/	/
	Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'	0.99999	99.99
	Mycobacterium tuberculosis CDC1551	0.99996	99.87
	Mycobacterium tuberculosis F11	0.99995	99.88
	Mycobacterium tuberculosis H37Ra	0.99995	99.88
	Mycobacterium tuberculosis KZN 1435	0.99998	99.91
T	Mycobacterium tuberculosis H37Rv	/	/
T	Mycoplasma hyopneumoniae J	/	/
	Mycoplasma hyopneumoniae 7448	0.99796	98.12
	Mycoplasma hyopneumoniae 232	0.9986	98.47
T	Rhizobium etli CFN 42	/	/
	Rhizobium etli CIAT 652	**0.99881**	**90.44**
	Rickettsia bellii OSU 85-389	0.99986	99.52
T	Rickettsia bellii RML369-C	/	/
T	Rickettsia rickettsii str. 'Sheila Smith'	/	/
	Rickettsia rickettsii str. Iowa	0.99992	99.86
T	Rhodobacter sphaeroides 2.4.1	/	/
	Rhodobacter sphaeroides ATCC 17025	**0.97495**	**87.63**
	Rhodobacter sphaeroides ATCC 17029	0.99965	98.01
	Rhodobacter sphaeroides KD131	0.99947	97.25
	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--	**0.99774**	**93.74**
	Salmonella enterica subsp. enterica serovar Agona str. SL483	0.99959	98.68
	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67	0.99969	98.81
	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853	0.99988	98.87
	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109	0.99968	98.92
	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91	0.99972	98.85
	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476	0.99982	99.08
	Salmonella enterica subsp. enterica serovar Newport str. SL254	0.99964	98.95
	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601	0.99966	98.55
	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	0.99967	98.54
	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7	0.99963	98.96
	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594	0.99979	98.86
	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633	0.99977	98.47
	Salmonella enterica subsp. enterica serovar Typhi str. Ty2	0.99977	98.43
T	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2	/	/
	Thermus thermophilus HB27	0.99966	98.84
T	Thermus thermophilus HB8	/	/
	Tropheryma whipplei TW08/27	0.99953	99.16
T	Tropheryma whipplei str. Twist	/	/
	Xanthomonas campestris pv. campestris str. 8004	0.99994	99.82
T	Xanthomonas campestris pv. campestris str. ATCC 33913 (LMG 658t)	/	/
	Xanthomonas campestris pv. campestris str. B100	0.99979	98.71
	Xanthomonas campestris pv. vesicatoria str. 85-10	**0.99277**	**87.6**

B- Analysis of ANIm and TETRA among the strains sharing specific name and for which no type strain is present. A reference strain has been used for the calculations (R)

R	Acinetobacter baumannii AB0057	/	/	**0.95369**	97.87		
	Acinetobacter baumannii AB307-0294	0.99878	99.68	**0.9529**	97.98		
	Acinetobacter baumannii ACICU	0.99876	97.83	**0.95224**	98.02		
	Acinetobacter baumannii ATCC 17978	0.99853	97.73	**0.95246**	97.97		
	Acinetobacter baumannii AYE	0.99951	99.7	**0.95255**	97.98		
	Acinetobacter baumannii SDF	**0.95369**	97.87	/	/		
R	Actinobacillus pleuropneumoniae L20	/	/				
	Actinobacillus pleuropneumoniae serovar 3 str. JL03	0.99965	98.38				
	Actinobacillus pleuropneumoniae serovar 7 str. AP76	0.99943	98.36				
R	Anaplasma marginale str. Florida	/	/				
	Anaplasma marginale str. St. Maries	0.99918	98.95				
R	Bacillus anthracis str. 'Ames Ancestor'	/	/				
	Bacillus anthracis str. Ames	0.99985	99.92				
	Bacillus anthracis CDC 684	0.99999	99.9				
	Bacillus anthracis str. Sterne	0.99985	99.9				
R	Bacillus thuringiensis serovar konkukian str. 97-27	/	/				
	Bacillus thuringiensis str. Al Hakam	0.99965	97.59				
R	Bifidobacterium longum DJO10A	/	/				
	Bifidobacterium longum NCC2705	0.99912	98.71				
R	Burkholderia pseudomallei 1106a	/	/				
	Burkholderia pseudomallei 1710b	0.99983	99.2				
	Burkholderia pseudomallei 668	0.99992	98.88				
	Burkholderia pseudomallei K96243	0.99988	99.15				
R	Campylobacter jejuni RM1221						
	Campylobacter jejuni subsp. doylei 269.97	0.99712	96.08				
	Campylobacter jejuni subsp. jejuni 81-176	0.9988	98.14				
	Campylobacter jejuni subsp. jejuni 81116	0.99824	97.83				
	Campylobacter jejuni subsp. jejuni NCTC 11168	0.99854	98.52				
R	Clavibacter michiganensis subsp. michiganensis NCPPB 382	/	/				
	Clavibacter michiganensis subsp. sepedonicus	**0.99759**	**92.44**				
R	Clostridium botulinum A str. ATCC 19397	/	/	**0.91685**	**84.74**	**0.90764**	**82.37**
	Clostridium botulinum A str. ATCC 3502	0.99989	99.84	**0.91803**	**84.76**	**0.90887**	**82.37**
	Clostridium botulinum A str. Hall	0.99994	99.93	**0.91545**	**84.76**	**0.90627**	**82.33**
	Clostridium botulinum A2 str. Kyoto	0.99913	97.8	**0.92127**	**83.56**	**0.91172**	**83.09**
	Clostridium botulinum A3 str. Loch Maree	0.9986	96.47	**0.92309**	**83.22**	**0.91321**	**83.12**
	Clostridium botulinum B str. Eklund 17B	**0.91685**	**84.74**	**/**	**/**	**0.99828**	**94.02**
	Clostridium botulinum B1 str. Okra	0.99907	97.44	**0.92155**	**85.61**	**0.91212**	**83.11**
	Clostridium botulinum E3 str. Alaska E43	**0.90764**	**82.37**	**0.99828**	**94.02**	**/**	**/**
	Clostridium botulinum F str. Langeland	0.99944	97.47	**0.91933**	**83.23**	**0.91008**	**83.01**

Note: strains Eklund 17B and Alaska E43 may be considered in the same genospecies, but different from that harbouring the rest of the strains analysed.

R	Coxiella burnetii CbuG_Q212	/	/				
	Coxiella burnetii CbuK_Q154	0.99913	99.36				
	Coxiella burnetii Dugway 5J108-111	0.99926	99.42				
	Coxiella burnetii RSA 331	0.99923	99.42				
	Coxiella burnetii RSA 493	0.99978	99.47				
R	Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774	/	/				
	Desulfovibrio desulfuricans subsp. desulfuricans str. G20	**0.78456**	**82.72**				
R	Escherichia coli 536	/	/				
	Escherichia coli 55989	0.99924	97.06				
	Escherichia coli APEC O1	0.99941	98.77				

	Escherichia coli ATCC 8739	0.99855	97.18		
	Escherichia coli CFT073	0.99955	98.78		
	Escherichia coli E24377A	0.99892	97.0		
	Escherichia coli ED1a	0.99875	98.75		
	Escherichia coli HS	0.99849	97.15		
	Escherichia coli IAI1	0.9984	97.16		
	Escherichia coli IAI39	0.99904	97.5		
	Escherichia coli O127:H6 str. E2348/69	0.99934	98.57		
	Escherichia coli O157:H7 EDL933	0.99779	97.04		
	Escherichia coli O157:H7 str. EC4115	0.99709	96.99		
	Escherichia coli O157:H7 str. Sakai	0.99764	96.99		
	Escherichia coli S88	0.9996	98.69		
	Escherichia coli SE11	0.9991	97.1		
	Escherichia coli SMS-3-5	0.99947	97.42		
	Escherichia coli UMN026	0.99898	97.19		
	Escherichia coli UTI89	0.99967	98.9		
	Escherichia coli str. K-12 substr. DH10B	0.99847	97.19		
	Escherichia coli str. K-12 substr. MG1655	0.99844	97.15		
	Escherichia coli str. K-12 substr. W3110	0.99848	97.17		
	Escherichia coli B str. REL606	0.99888	97.14		
	Escherichia coli BL21	0.99824	97.17		
	Escherichia coli BL21(DE3)	0.99823	97.18		
	Escherichia coli BW2952	0.99865	97.16		
	Escherichia coli O157:H7 str. TW14359	0.99747	96.99		
R	Francisella tularensis subsp. holarctica	/	/		
	Francisella tularensis subsp. holarctica FTNF002-00	0.99989	99.89		
	Francisella tularensis subsp. holarctica OSU18	0.99993	99.87		
	Francisella tularensis subsp. mediasiatica FSC147	0.99791	99.25		
	Francisella tularensis subsp. tularensis FSC198	0.99881	99.31		
	Francisella tularensis subsp. tularensis SCHU S4	0.9988	99.31		
	Francisella tularensis subsp. tularensis WY96-3418	0.99876	99.39		
R	Haemophilus influenzae 86-028NP	/	/		
	Haemophilus influenzae PittEE	0.99899	97.3		
	Haemophilus influenzae PittGG	0.9991	97.31		
	Haemophilus influenzae Rd KW20	0.99869	97.36		
R	Helicobacter pylori 26695	/	/		
	Helicobacter pylori G27	0.99962	95.36		
	Helicobacter pylori HPAG1	0.99959	95.47		
	Helicobacter pylori J99	0.99849	93.92		
	Helicobacter pylori P12	0.99961	95.34		
	Helicobacter pylori Shi470	0.99876	94.54		
	Helicobacter pylori B38	0.99936	95.19		
R	Klebsiella pneumoniae 342	/	/	**0.99878**	**94.76**
	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	**0.99878**	**94.76**	/	/
	Klebsiella pneumoniae NTUH-K2044	**0.99813**	**94.75**	0.99936	99.18
R	Lactobacillus casei ATCC 334	/	/		
	Lactobacillus casei BL23	0.99746	98.68		
R	Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842	/	/		
	Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365	0.99978	99.02		
R	Lactococcus lactis subsp. cremoris MG1363	/	/		
	Lactococcus lactis subsp. cremoris SK11	0.99773	97.97		
	Lactococcus lactis subsp. lactis Il1403	**0.99422**	**88.55**		
R	Lactobacillus plantarum WCFS1	**/**	**/**		
	Lactobacillus plantarum JDM1	0.99903	99.1		

R	Leptospira borgpetersenii serovar Hardjo-bovis JB197	/	/				
	Leptospira borgpetersenii serovar Hardjo-bovis L550	0.99989	99.62				
R	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	/	/				
	Leptospira interrogans serovar Lai str. 56601	0.99939	99.03				
R	Listeria monocytogenes EGD-e	/	/	**0.99809**	**93.55**	**0.99885**	**94.86**
	Listeria monocytogenes HCC23	**0.99809**	**93.55**	**/**	**/**	**0.99868**	**95.08**
	Listeria monocytogenes str. 4b F2365	**0.99885**	**94.86**	**0.99868**	**95.08**	**/**	**/**
R	Methanococcus maripaludis C5	/	/	**0.99575**	**91.7**	**0.99674**	**90.58**
	Methanococcus maripaludis C6	**0.9957**	**90.9**	**/**	**/**	**0.99834**	**90.92**
	Methanococcus maripaludis C7	**0.99655**	**89.69**	**0.99834**	**90.93**	**/**	**/**
	Methanococcus maripaludis S2	**0.96206**	**76.76**	**0.99242**	**89.02**	**0.99263**	**88.49**
R	Methylobacterium extorquens PA1	**/**	**/**				
	Methylobacterium extorquens AM1	0.99669	96.94				
	Methylobacterium extorquens DM4	0.99934	97.03				
R	Mycobacterium avium 104	/	/				
	Mycobacterium avium subsp. paratuberculosis K-10	0.99956	98.7				
R	Mycobacterium bovis AF2122/97	/	/				
	Mycobacterium bovis BCG str. Pasteur 1173P2	0.99998	99.91				
	Mycobacterium bovis BCG str. Tokyo 172	0.99998	99.91				
R	Mycobacterium leprae Br4923	/	/				
	Mycobacterium leprae TN	1	99.98				
R	Neisseria gonorrhoeae FA 1090	/	/				
	Neisseria gonorrhoeae NCCP11945	0.99975	99.09				
R	Neisseria meningitidis 053442	/	/				
	Neisseria meningitidis FAM18	0.99973	97.28				
	Neisseria meningitidis MC58	0.99967	97.11				
	Neisseria meningitidis Z2491	0.99967	97.18				
R	Orientia tsutsugamushi str. Boryong	/	/				
	Orientia tsutsugamushi str. Ikeda	0.98609	94.49				
R	Polynucleobacter necessarius subsp. asymbioticus QLW-P1DMWA-1	/	/				
	Polynucleobacter necessarius subsp. necessarius STIR1	**0.97442**	**84.08**				
R	Pseudomonas aeruginosa LESB58	/	**/**				
	Pseudomonas aeruginosa PA7	0.9972	93.75				
	Pseudomonas aeruginosa PAO1	0.99985	99.39				
	Pseudomonas aeruginosa UCBPP-PA14	0.99987	98.8				
R	Pseudomonas fluorescens Pf-5	/	/				
	Pseudomonas fluorescens Pf0-1	**0.92411**	**85.73**				
R	Pseudomonas putida F1	/	/	**0.99553**	**87.42**	**0.99039**	**87.4**
	Pseudomonas putida GB-1	**0.99553**	**91.18**	**/**	**/**	**0.98982**	**87.42**
	Pseudomonas putida KT2440	0.99912	97.06	**0.99657**	**91.08**	**0.99091**	**87.33**
	Pseudomonas putida W619	**0.99091**	**87.96**	**0.98982**	**91.15**	**/**	**/**
	Note: in this group only F1 and KT2440 belong to the same genospecies						
R	Pseudomonas syringae pv. phaseolicola 1448A	/	/	**0.98859**	**89.67**	**0.98877**	**88.25**
	Pseudomonas syringae pv. syringae B728a	**0.98859**	**89.67**	**/**	**/**	**0.99091**	**87.96**
	Pseudomonas syringae pv. tomato str. DC3000	**0.98877**	**88.26**	**0.99091**	**87.96**	**/**	**/**
R	Prochlorococcus marinus str. AS9601	**0.94131**	**85.85**				
	Prochlorococcus marinus str. MIT 9211	**0.9293**	**88.02**				
	Prochlorococcus marinus str. MIT 9215	**0.93891**	**87.22**				
	Prochlorococcus marinus str. MIT 9301	**0.94259**	**86.67**				
	Prochlorococcus marinus str. MIT 9303	**0.77552**	**93.07**				
	Prochlorococcus marinus str. MIT 9312	**0.94137**	**88.75**				
	Prochlorococcus marinus str. MIT 9313	**0.75482**	**93.04**				
	Prochlorococcus marinus str. MIT 9515	**0.94995**	**89.2**				
	Prochlorococcus marinus str. NATL1A	**0.99802**	**97.18**				

R	Prochlorococcus marinus str. NATL2A	**/**	**/**				
	Note: none of the genomes analyzed shared values above 96% ANI all the genomes studied were distantly related with values ranging 93.8 – 82%						
R	Ralstonia eutropha H16 (correct name Cupriavidus pinatubonensis)	**/**	**/**				
	Ralstonia eutropha JMP134 (correct name Cupriavidus pinatubonensis)	**0.96848**	**86.52**				
R	Ralstonia pickettii 12J	/	/				
	Ralstonia pickettii 12D	0.99918	95.98				
R	Rhizobium leguminosarum bv. trifolii WSM2304	/	/				
	Rhizobium leguminosarum bv. viciae 3841	**0.99783**	**89.34**				
R	Rhodopseudomonas palustris BisA53	/	/	**0.98269**	**84.86**	**0.9907**	**85.93**
	Rhodopseudomonas palustris BisB18	**0.9907**	**85.93**	**0.98061**	**84.65**	**/**	**/**
	Rhodopseudomonas palustris BisB5	**0.98576**	**85.31**	**0.9873**	**86.16**	**0.98201**	**85.04**
	Rhodopseudomonas palustris CGA009	**0.98279**	**84.81**	0.98931	97.82	**0.98082**	**84.89**
	Rhodopseudomonas palustris HaA2	**0.98723**	**85.42**	**0.99969**	**86.18**	**0.98412**	**85.22**
	Rhodopseudomonas palustris TIE-1	**0.98269**	**84.86**	**/**	**/**	**0.98061**	**84.64**
R	Shewanella baltica OS155	/	/				
	Shewanella baltica OS185	0.99877	96.9				
	Shewanella baltica OS195	0.99876	96.81				
	Shewanella baltica OS223	0.99856	97.1				
R	Shigella boydii CDC 3083-94	/	/				
	Shigella boydii Sb227	0.99815	99.54				
R	Shigella flexneri 2a str. 2457T	/	/				
	Shigella flexneri 2a str. 301	0.99963	99.82				
	Shigella flexneri 5 str. 8401	0.99991	99.73				
R	Staphylococcus aureus RF122	/	/				
	Staphylococcus aureus subsp. aureus COL	0.99922	97.89				
	Staphylococcus aureus subsp. aureus JH1	0.99887	97.85				
	Staphylococcus aureus subsp. aureus JH9	0.99886	97.85				
	Staphylococcus aureus subsp. aureus MRSA252	0.99893	97.7				
	Staphylococcus aureus subsp. aureus MSSA476	0.99928	97.96				
	Staphylococcus aureus subsp. aureus MW2	0.99933	97.97				
	Staphylococcus aureus subsp. aureus Mu3	0.99908	97.88				
	Staphylococcus aureus subsp. aureus Mu50	0.99908	97.87				
	Staphylococcus aureus subsp. aureus N315	0.99919	97.94				
	Staphylococcus aureus subsp. aureus NCTC 8325	0.99939	97.87				
	Staphylococcus aureus subsp. aureus USA300_FPR3757	0.99897	97.88				
	Staphylococcus aureus subsp. aureus USA300_TCH1516	0.99904	97.87				
	Staphylococcus aureus subsp. aureus str. Newman	0.99914	97.81				
R	Staphylococcus epidermidis ATCC 12228	/	/				
	Staphylococcus epidermidis RP62A	0.99851	99.24				
R	Stenotrophomonas maltophilia K279a	/	/				
	Stenotrophomonas maltophilia R551-3	**0.99849**	**91.35**				
	Note: both strains do not belong to the same genospecies						
R	Streptococcus agalactiae 2603V/R	/	/				
	Streptococcus agalactiae A909	0.99897	99.43				
	Streptococcus agalactiae NEM316	0.99797	99.41				
R	Streptococcus equi subsp. equi 4047	/	/				
	Streptococcus equi subsp. zooepidemicus	0.99638	96.8				
	Streptococcus equi subsp. zooepidemicus MGCS10565	0.99416	96.82				
R	Streptococcus pneumoniae 70585	/	/				
	Streptococcus pneumoniae ATCC 700669	0.99836	98.43				
	Streptococcus pneumoniae CGSP14	0.99843	98.42				
	Streptococcus pneumoniae D39	0.99853	98.47				
	Streptococcus pneumoniae G54	0.99855	98.48				

	Streptococcus pneumoniae Hungary19A-6	0.9978	98.23
	Streptococcus pneumoniae JJA	0.99918	98.44
	Streptococcus pneumoniae P1031	0.99877	98.58
	Streptococcus pneumoniae R6	0.99853	98.47
	Streptococcus pneumoniae TIGR4	0.99784	98.45
	Streptococcus pneumoniae Taiwan19F-14	0.9983	98.4
R	Streptococcus pyogenes M1 GAS	/	/
	Streptococcus pyogenes MGAS10270	0.99888	98.74
	Streptococcus pyogenes MGAS10394	0.99872	98.5
	Streptococcus pyogenes MGAS10750	0.99899	98.65
	Streptococcus pyogenes MGAS2096	0.99789	98.84
	Streptococcus pyogenes MGAS315	0.99846	98.69
	Streptococcus pyogenes MGAS5005	0.99979	99.81
	Streptococcus pyogenes MGAS6180	0.99923	98.81
	Streptococcus pyogenes MGAS8232	0.99846	98.46
	Streptococcus pyogenes MGAS9429	0.99938	98.78
	Streptococcus pyogenes NZ131	0.99937	98.76
	Streptococcus pyogenes SSI-1	0.99845	98.66
	Streptococcus pyogenes str. Manfredo	0.99903	98.56
R	Streptococcus suis 05ZYH33	/	/
	Streptococcus suis 98HAH33	0.99992	99.62
	Streptococcus suis BM407	0.99962	99.58
	Streptococcus suis P1/7	0.99963	99.74
	Streptococcus suis SC84	0.9999	99.76
R	Streptococcus thermophilus CNRZ1066	/	/
	Streptococcus thermophilus LMD-9	0.99915	98.79
	Streptococcus thermophilus LMG 18311	0.99963	99.42
R	Synechococcus elongatus PCC 6301	0.99997	99.91
	Synechococcus elongatus PCC 7942	/	/
R	Treponema pallidum subsp. pallidum SS14	/	/
	Treponema pallidum subsp. pallidum str. Nichols	0.99994	99.92
R	Vibrio cholerae O1 biovar El Tor str. N16961	/	/
	Vibrio cholerae M66_2	0.99982	99.79
	Vibrio cholerae O395	0.99942	99.34
R	Vibrio fischeri ES114	/	/
	Vibrio fischeri MJ11	0.9991	95.82
R	Vibrio vulnificus CMCP6	/	/
	Vibrio vulnificus YJ016	0.99954	98.31
R	Xanthomonas oryzae pv. oryzae KACC10331	/	/
	Xanthomonas oryzae pv. oryzae MAFF 311018	0.99988	99.1
	Xanthomonas oryzae pv. oryzae PXO99A	0.99956	98.88
R	Xylella fastidiosa 9a5c	/	/
	Xylella fastidiosa M12	0.99574	96.03
	Xylella fastidiosa M23	0.99574	95.71
	Xylella fastidiosa Temecula1	0.99588	95.68
R	Yersinia pestis Angola	/	/
	Yersinia pestis Antiqua	0.99921	99.83
	Yersinia pestis CO92	0.99964	99.81
	Yersinia pestis KIM	0.99956	99.82
	Yersinia pestis Nepal516	0.99962	99.81
	Yersinia pestis Pestoides F	0.99934	99.79
	Yersinia pestis biovar Microtus str. 91001	0.99937	99.8
R	Yersinia pseudotuberculosis IP 31758	/	/
	Yersinia pseudotuberculosis IP 32953	0.99968	98.98

Yersinia pseudotuberculosis PB1/+	0.99961	98.96
Yersinia pseudotuberculosis YPIII	0.99958	99.03